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FIGURE 363

ACACTGGCCAAACAAAAACGAAAGCACTCCGTGCTGGAAGTAGGAGGAGAGTCAGGACTC
CCAGGACAGAGAGTGCACAACTACCCAGCACAGCCCCCTCCGCCCCCTCTGGAGGCTGA
AGAGGGATTCCAGCCCCCTGCCACCCACAGACACGGGCTGACTGGGGTGTCTGCCCCCTT
GGGGGGGGGCAGCACAGGGCCTCAGGCCTGGGTGCCACCTGGCACCTAGAAGATGCCTGT
GCCCTGGTTCTTGCTGTCTTGGCACTGGGCGGAAGCCAGTGGTCCTTTCTCTGGAGAG
GCTTGTGGGGCCTCAGGACGCTACCCACTGCTCTCCGGGCCTCTCCTGCCGCCTCTGGGA
CAGTGACATACTCTGCCTGCCTGGGGACATCGTGCCTGCTCCGGGCCCCGTGCTGGCGCC
TACGCACCTGCAGACAGAGCTGGTGCTGAGGTGCCAGAAGGAGACCGACTGTGACCTCTG
TCTGCGTGTGGCTGTCCACTTGGCCGTGCATGGGCACTGGGAAGAGCCTGAAGATGAGGA
AAAGTTTGGAGGAGCAGCTGACTCAGGGGTGGAGGAGCCTAGGAATGCCTCTCTCCAGGC
CCAAGTCGTGCTCTCCTTCCAGGCCTACCTACTGCCCGCTGCGTCCTGCTGGAGGTGCA
AGTGCCTGCTGCCCTTGTGCAGTTTGGTCAGTCTGTGGGCTCTGTGGTATATGACTGCTT
CGAGGCTGCCCTAGGGAGTGAGGTACGAATCTGGTCCATACTCAGCCCAGGTACGAGAA
GGAActCAACCACACACAGCAGCTGCCTGCCCTGCCCTGGCTCAACGTGTGAGCAGATGG
TGACAACGTGCATCTGGTTCTGAATGTCTCTGAGGAGCAGCACTTCGGCCTCTCCCTGTA
CTGGAATCAGTCCAGGGCCCCCCTAAACCCCGGTGGCACAAAAACCTGACTGGACCGCA
GATCATTACCTTGAACCACACAGACCTGGTTCCCTGCCTCTGTATTGAGGTGTGGCCTCT
GGAACCTGACTCCGTTAGGACGAACATCTGCCCTTCAGGGAGGACCCCCCGGCACACCA
GAACCTCTGGCAAGCCCGCCGACTGCGACTGCTGACCCTGCAGAGCTGGCTGCTGGACGC
ACCGTGCTCGCTGCCCGCAGAAGCGGCACTGTGCTGGCGGGCTCCGGGTGGGGACCCCTG
CCAGCCACTGGTCCACCGCTTTCTGGGAGAAGCTCACTGTGGACAAGGTTCTCGAGTT
CCCATTGCTGAAAGGCCACCCTAACCTCTGTGTTGAGGTGAACAGCTCGGAGAAGCTGCA
GCTGCAGGAGTGCTTGTGGGCTGACTCCCTGGGGCCTCTCAAAGACGATGTGCTACTGTT
GGAGACACGAGGCCCCCAGGACAACAGATCCCTCTGTGCCTTGGAACCCAGTGGCTGTAC
TTCATAACCCAGCAAAGCCTCCACGAGGGCAGCTCGCCTTGGAGAGTACTTACTACAAGA
CCTGCAGTCAGGCCAGTGTCTGCAGCTATGGGACGATGACTTGGGAGCGCTATGGGCCTG
CCCCATGGACAAATACATCCACAAGCGCTGGGCCCTCGTGTGGCTGGCCTGCCTACTCTT
TGCCGCTGCGCTTTCCCTCATCCTCCTTCTCAAAAAGGATCACGCGAAAGGGTGGCTGAG
GCTCTTGAAACAGGACGTCCGCTCGGGGGCGGCCGACGGGGCCGCGCGGCTCTGCTCCT
CTACTCAGCCGATGACTCGGGTTTCGAGCGCCTGGTGGGCGCCCTGGCGTGGGCCCTGTG
CCAGCTGCCGCTGCGCGTGGCCGTAGACCTGTGGAGCCGTCGTGAACTGAGCGCGCAGGG
GCCCCGTGGCTTGGTTTACGCGCAGCGGCGCCAGACCCTGCAGGAGGGCGGCGTGGTGGT
CTTGCTCTTCTCTCCCGGTGCGGTGGCGCTGTGCAGCGAGTGGCTACAGGATGGGGTGTG
CGGGCCCCGGGGCGCACGGCCCCGACGACGCTTCCGCGCCTCGCTCAGCTGCGTGCTGCC
CGACTTCTTGACAGGGCCGGGGCGCCCGGACGCTACGTGGGGGCCTGCTTCGACAGGCTGCT
CCACCCGGACGCGGTACCCGCCCTTTTCCGACCCGTGCCCGTCTTCACACTGCCCTCCCA
ACTGCCAGACTTCTGGGGGCCCTGCAGCAGCCTCGCGCCCCGCGTTCCGGGCGGCTCCA
AGAGAGAGCGGAGCAAGTGTCCCGGGCCCTTCAGCCAGCCCTGGATAGCTACTTCCATCC
CCCGGGGACTCCCGCGCCGGGACGCGGGGTGGGACCAGGGGCGGGACCTGGGGCGGGGA
CGGGACTTAAATAAAGGCAGACGCTGTTTTTCTAAAAAA

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FIGURE 364

MPVPWFLLSLALGRSPVVLSELERLVGPQDATHCSPGLSCRLWDS DILCLPGDIVPAPGPV
LAPTHLQTELVLRCQKETDCDLCLRVAVHLAVHGHWEPEDEEKFGGAADSGVEEPRNAS
LQAQVVL SFQAYPTARCVLLEVQVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTQPR
YEKELNHTQQLPALPWLNV SADGDNVHLVLNVSEEQHFGLSLYWNQVQGP PKPRWHKNLT
GPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLRLLTLQSWL
LDAPCSLPAAEALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQVNSSE
KLQEQECLWADSLGPLKDDVLLLETRGPQDNRS LCALEPSGCTSLPSKASTRAARLGEYL
LQDLQSGQCLQLWDDDLGALWACPMDKYIHKRWALVWLACLLFAAALSLILLKKDHAKG
WLRLKQDVRS GAAARGRAALLLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELS
AQGPVAWFHAQRRQTLQEGGVVLLFSPGAVALCSEWLQDGVSGPGAHGPHDAFRASLSC
VLPDFLQGRAPGSYVGACFDRL LHPPDAVPALFRTVPVFTLPSQLPDFL GALQQPRAPRSG
RLQERAEQVSRALQPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT

Signal sequence:
amino acids 1-20

Transmembrane domain:
amino acids 453-475

N-glycosylation sites:
amino acids 118-121, 186-189, 198-201, 211-214, 238-241,
248-251, 334-337, 357-360, 391-394

Glycosaminoglycan attachment site:
amino acids 583-586

cAMP- and cGMP-dependent protein kinase phosphorylation site:
amino acids 552-555

N-myristoylation sites:
amino acids 107-112, 152-157, 319-324, 438-443, 516-521,
612-617, 692-697, 696-701, 700-705

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FIGURE 365

AATAGAAGTCCTCAGGACGGAGCAGAGGTGGCCGGCGGGCCCGGCTGACTGCGCCTCTGC
TTTCTTTCCATAACCTTTTCTTTTCGGACTCGAATCACGGCTGCTGCGAAGGGTCTAGTTC
CGGACACTAGGGTGCCCGAACGCGCTGATGCCCCGAGTGCTCGCAGGGCTTCCCGCTAAC
CATGCTGCCGCGCGCGGGCCCGCAGCTGCCTTGCGCTGCCTGTGCTCCTGCTACTGCT
GGTGGTGCTGACGCCGCCCCGACCGGCGCAAGGCCATCCCCAGGCCAGATTACCTGCG
GCGCGGCTGGATGCGGCTGCTAGCGGAGGGCGAGGGCTGCGCTCCCTGCCGGCCAGAAGA
GTGCGCCGCGCGCGGGGCTGCCTGGCGGGCAGGGTGCGCGACGCGTGCGGCTGCTGCTG
GGAATGCGCCAACCTCGAGGGCCAGCTCTGCGACCTGGACCCCACTGCTCACTTCTACGG
GCACTGCGGCGAGCAGCTTGAGTGCCGGCTGGACACAGGCGGGCGACCTGAGCCGCGGAGA
GGTGCCGGAACCTCTGTGTGCCTGTGCTTCGCGAGAGTCCGCTCTGCGGGTCCGACGGTCA
CACCTACTCCCAGATCTGCCGCTGCAGGAGGCGGCCCCGCGCTCGGCCCGATGCCAACCT
CACTGTGGCACACCCGGGGCCCTGCGAATCGGGGCCCCAGATCGTGTCACATCCATATGA
CACTTGGAATGTGACAGGGCAGGATGTGATCTTTGGCTGTGAAGTGTTCCTACCCCAT
GGCCTCCATCGAGTGAGGAAGGATGGCTTGACATCCAGCTGCCAGGGGATGACCCCA
CATCTCTGTGCAGTTTAGGGGTGGACCCAGAGGTTTGAGGTGACTGGCTGGCTGCAGAT
CCAGGCTGTGCGTCCCAGTGATGAGGGCACTTACCGCTGCCTTGCCGCAATGCCCTGGG
TCAAGTGAGGCCCCCTGCTAGCTTGACAGTGCTCACACCTGACCAGCTGAACTCTACAGG
CATCCCCCAGCTGCGATCACTAAACCTGGTTCCCTGAGGAGGAGGCTGAGAGTGAAGAGAA
TGACGATTACTACTAGGTCCAGAGCTCTGGCCCATGGGGGTGGGTGAGCGGCTATAGTGT
TCATCCCTGCTCTTGAAAAGACCTGGAAAGGGGAGCAGGGTCCCTTCATCGACTGCTTTC
ATGCTGTGCTAGGGATGATCATGGGAGGCCTATTTGACTCCAAGGTAGCAGTGTGGTAG
GATAGAGACAAAAGCTGGAGGAGGGTAGGGAGAGAAGCTGAGACCAGGACCGGTGGGGTA
CAAAGGGGCCCATGCAGGAGATGCCCTGGCCAGTAGGACCTCCAACAGGTTGTTTCCCAG
GCTGGGGTGGGGGCCTGAGCAGACACAGAGGTGCAGGCACCAGGATTCTCCACTTCTTCC
AGCCCTGCTGGGCCACAGTTCTAACTGCCCTTCCTCCCAGGCCCTGGTTCTTGCTATTTC
CTGGTCCCCAACGTTTATCTAGCTTGTTTGCCCTTTCCCCAACTCATCTTCCAGAACTT
TTCCCTCTCTCCTAAGCCCCAGTTGCACCTACTAACTGCAGTCCCTTTTGCTGTCTGCCG
TCTTTTGTACAAGAGAGAGAAACAGCGGAGCATGACTTAGTTCAGTGCAGAGAGATTT

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FIGURE 366

MLPPPRPAAALALPVLLLLLVLTTPPPTGARPSGPDYLRGWMRLLAEGEGCAPCRPEE
CAAPRGCLAGRVRDAGCCWECANLEGQLCDLDPSAHFYGHCGEQLECRDLDGDLRGE
VPEPLCACRSQSPLCGSDGHTYSQICRLQEAARARPDANLTVAHPGPCESGPQIVSHPYD
TWNVTGQDVIFGCEVFAYPMASIEWRKDGLDIQLPGDDPHISVQFRGGPQRFVETGWLQI
QAVRPSDEGTYRCLGRNALGQVEAPASLTVLTPDQLNSTGIPQLRSLNLVPEEEAESEEN
DDYY

Important features of the protein:

Signal peptide:

1-30

Transmembrane domain:

None

N-glycosylation site:

159-163, 183-187, 277-281

Tyrosine kinase phosphorylation site:

244-252

N-myristoylation site:

52-58, 66-72, 113-119, 249-255

Kazal-type serine protease inhibitor domain:

121-168

Immunoglobulin domain:

186-255

Insulin-like growth factor binding proteins:

53-90

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FIGURE 367

AGACGCTACAGGATGGAGCGGGGCGCAGGAGCCAAGCTGCTGCCGCTGCTGCTGCTTCTG
CGGGCGACTGGTTTTACATGTGCACAGACAGATGGCCGGAACGGCTACACGGCGGTCATC
GAAGTGACCAGCGGGGGTCCCTGGGGCGACTGGGCCTGGCCTGAGATGTGTCCCGATGGA
TTCTTCGCCAGCGGGTTCTCGCTCAAGGTGGAGCCTCCCCAAGGCATTCTTGGCGACGAC
ACTGCACTGAATGGGATCAGGCTGCACTGCGCGCGCGGGAACGTCCTAGGCAATACGCAC
GTGGTAGAGTCCAGTCTGGAAGCTGGGGCGAATGGAGTGAGCCGCTGTGGTGTGCGCGC
GGCGCCTACCTAGTGGCTTTCTCGCTTCGCGTGGAGGCACCCACGACCCTCGGTGACAAC
ACAGCAGCGAACAACGTGCGCTTCCGCTGTTTCAGACGGCGAGGAAGTGCAGGGGCCTGGG
CTGAGCTGGGGAGACTTTGGAGACTGGAGTGACCATTGCCCAAGGGCGCGTGCGGCCTG
CAGACCAAGATCCAGGGACCTAGAGGCCTCGGCGATGACACTGCGCTGAACGACGCGCGC
TTATTCTGCTGCCGCAGTGAACGGCGCCGCCGCCGCTCTCTCCCGGGCCAGGAGGC
TAGTCCCACCTCTTGCTATTAAAGCTTCTCTGAGTTG

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FIGURE 368

MERGAGAKLLPLLLLLLRATGFTCAQTDGRNGYTAVIEVTSGGPWGDWAWPEMCPDGFFAS
GFSLKVEPPQGIPGDDTALNGIRLHCARGNVLGNTHVVESQSGSWGGEWSEPLWCRGGAYL
VAFSLRVEAPTTLGDNNTAANNVRFRCSDEELQGPGLSWGDFGDWSDHCPKGACGLQTKI
QGPRGLGDDTALNDARLFCCRS

Important features of the protein:

Signal peptide:

1-24

Transmembrane domain:

None

N-myristoylation site:

41-47

89-95

156-162

Growth factor and cytokines receptors family signature 2:

103-110

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FIGURE 369

GCCAACACTGGCCAAACCTCGGAGACCGTCCTGCGCTCTCTGGAGACGCGCTGTCCGCGC
CCAGGGTGGTGCCATGTGGGGCGCTCGCCGCTCGTCCGTCTCCTCATCCTGGAACGCCGC
TTCGCTCCTGCAGCTGCTGCTGGCTGCGCTGCTGGCGGCGGGGGCGAGGGCCAGCGCGA
GTACTGCCACGGCTGGCTGGACGCGCAGGGCGTCTGGCGCATCGGCTTCCAGTGTCCCGA
GCGCTTCGACGGCGGGCGACGCCACCATCTGCTGCGGCAGCTGCGCGTTGCGCTACTGCTG
CTCCAGCGCCGAGGCGCGCCTGGACCAGGGCGGCTGCGACAATGACCGCCAGCAGGGCGC
TGGCGAGCCTGGCCGGGCGGACAAAGACGGCCCCGACGGCTCGGCAGTGCCCATCTACGT
GCCGTTCCCTCATTTGTTGGCTCCGTGTTTGTGCGCTTTATCATCTTGGGGTCCCTGGTGGC
AGCCTGTTGCTGCAGATGTCTCCGGCCTAAGCAGGATCCCCAGCAGAGCCGAGCCCCAGG
GGGTAACCGCTTGATGGAGACCATCCCCATGATCCCCAGTGCCAGCACCTCCCGGGGGTTC
GTCCTCAGCCAGTCCAGCACAGCTGCCAGTTCCAGCTCCAGCGCCAACTCAGGGGCCCCG
GGCGCCCCCAACAAGGTCACAGACCAACTGTTGCTTGCCGGAAGGGACCATGAACAACGT
GTATGTCAACATGCCCACGAATTTCTCTGTGCTGAACTGTCAGCAGGCCACCCAGATTGT
GCCACATCAAGGGCAGTATCTGCATCCCCCATACTGTTGGGTACACGGTGCAGCACGACTC
TGTGCCCATGACAGCTGTGCCACCTTTCATGGACGGCCTGCAGCCTGGCTACAGGCAGAT
TCAGTCCCCCTTCCCTCACACCAACAGTGAACAGAAGATGTACCCAGCGGTGACTGTATA
ACCGAGAGTCACTGGTGGGTTCCTTTACTGAAGGGAGACGAAGGCAGGGGTGGATTTTCG
AGGTGGAAGT

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FIGURE 370

MWGARRSSVSSSWNAASLLQLLLAALLAAGARASGEYCHGWLDAQGVWRIGFQCPERFDG
GDATICCGSCALRYCCSSAEARLDQGGCDNDRQQGAGEPGRADKDGPDGSAVPIYVPFLI
VGSVFVAFIILGSLVAACCCRCLRPKQDPQQSRAPGGNRLMETIPMIPSASTSRGSSSRQ
SSTAASSSSSANS GARAPPTRSQTNCCLPEGTMNNVYVNMPTNFSVLNCQQATQIVPHQG
QYLHPPYVGYTVQHDSVPMTAVPPFMDGLQPGYRQIQSPFPHTNSEQKMYPAVTV

Important features of the protein: .

Signal peptide:

1-33

Transmembrane domain:

54-78

N-glycosylation site:

223-226

cAMP- and cGMP-dependent protein kinase phosphorylation site:

5-8

N-myristoylation site:

3-8, 30-35, 60-65, 86-91, 132-137, 211-216, 268-273

Prokaryotic membrane lipoprotein lipid attachment site:

128-138

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FIGURE 371

CACCAGACAGCACTCCAGCACTCTGTTTTGGGGGGCATTTCGAAACAGCAAAATCACTCATA
AAAGGCAGAAAAATTGCAAAAAAATAGTAATAACCAGCATGGCACTAAATAGACCATGA
AAAGACATGTGTGTGCAGTATGAAAATTGAGACAGGAAGGCAGAGTGTCTAGCTTGTTC
CCTCAGCTGGGAATGTGCATCAGGCAACTCAAGTTTTTCACCACGGCATGTGTCTGTGAA
TGTCCGCAAAACATTCTCTCTCCCCAGCCTTCATGTGTTAACCTGGGGATGATGTGGACC
TGGGCACTGTGGATGCTCCCTTCACTCTGCAAATTCAGCCTGGCAGCTCTGCCAGCTAAG
CCTGAGAACATTTCTGTGTCTACTACTATAGGAAAAATTTAACCTGCCTTGGAGTCCA
GGAAAGGAAACCAGTTATACCCAGTACACAGTTAAGAGAACTTACGCTTTTGGAGAAAAA
CATGATAATTGTACAACCAATAGTTCTACAAGTGAAAAATCGTGCTTCGTGCTCTTTTTC
CTTCCAAGAATAACGATCCCAGATAATTATACCATGAGGTGGAAGCTGAAAAATGGAGAT
GGTGTAAATTAATCTCATATGACATACTGGAGATTAGAGAACATAGCGAAAACTGAACCA
CCTAAGATTTTCCGTGTGAAACAGTTTTTGGGCATCAAACGAATGATTCAAATTGAATGG
ATAAAGCCTGAGTTGGCGCCTGTTTCATCTGATTTAAAAATACACACTTCGATTCAGGACA
GTCAACAGTACCAGCTGGATGGAAGTCAACTTCGCTAAGAACCGTAAGGATAAAAAACCAA
ACGTACAACCTCACGGGGCTGCAGCCTTTTACAGAATATGTCATAGCTCTGCGATGTGCG
GTCAAGGAGTCAAAGTCTGGAGTGACTGGAGCCAAGAAAAAATGGGAATGACTGAGGAA
GAAGCTCCATGTGGCCTGGAACCTGTGGAGAGTCCTGAAACCAGCTGAGGCGGATGGAAGA
AGGCCAGTGCGTTGTTATGGAAGAAGGCAAGAGGAGCCCCAGTCCTAGAGAAAAACACTT
GGCTACAACATATGGTACTATCCAGAAAGCAACACTAACCTCACAGAAACAATGAACACT
ACTAACAGCAGCTTGAACCTGCATCTGGGAGGCGAGAGCTTTTGGGTGTCTATGATTTCT
TATAATTCTCTTGGGAAGTCTCCAGTGGCCACCCTGAGGATTCCAGCTATTCAAGAAAAA
TCATTTTCAGTGCATTGAGGTCTGCAGGCGCTGCGTTGCTGAGGACCAGCTGGGTGAAG
TGGCAAAGCTCTGCTCTAGACGTGAACACTTGGATGATTGAATGGTTTCCGGATGTGGAC
TCAGAGCCCACCACCTTTCTGGAATCTGTGTCTCAGGCCACGAACCTGGACGATCCAG
CAAGATAAATTAACCTTTCTGTTGCTATAACATCTCTGTGTATCCAATGTTGCATGAC
AAAGTTGGCGAGCCATATTCATCCAGGCTTATGCCAAAGAAGGCGTTCCATCAGAAGGT
CCTGAGACCAAGGTGGAGAACATTGGCGTGAAGACGGTCACGATCACATGGAAAGAGATT
CCCAAGAGTGAGAGAAAGGGTATCATCTGCAACTACACCATCTTTTACCAAGCTGAAGGT
GGAAAAGGATTCTGTAAGCACGCCATAGCGAAGTGGAAGAAAAACCCCAAGCCCCAGATA
GATGCTATGGATAGACCTGTTGTAGGCATGGCTCCCCCATCTCATTGTGACTTGCAACCT
GGCATGAATCACTTAGCTTCTTTAAATCTCTCTGAAAATGGGGCCAAGAGCACCCACCTT
TTGGGGTTTTGGGGTTAAATGAGAGTGAAGTGACAGTACCTGAGAGGAGAGTCTGAGG
AAATGGAAGGAGTTGTTATAATTTGTCTGTTAGGCCCTGAATTGACCTCCCGGGAGCT
CCCCGACCATCATTCCCAGGAATGGCGTGCCTGGCTTAAAGAGTGAGGAGGAACAGACCC
TGTCACCATGACTTCTACTGCCCCCTGCCAATCATGCTTTTGTTTTTTCAGTCCACCTTAT
CTCCTGACATCTTAAATACTGGGCAAGGCTTGGATTCTTGCTTAGGCTAAATAATTTTTT
CTTATGGTAAAAATACAGTAAAAATTTTTCCAGTTTAAACATTTGAAAGTGTAATTTT
AGTGGCATTAGAAGCATTACAATATTGTGCAACCATCACCCTATTTCCAGAACTCTTC
TATTTCTGCCCCAAATAGAAGCCCTATACCCATTATTAGTCACTCCCATTCCTCTCCTC
CCACAGCCCCTGGCAACTACCAAACTGCTTTGTGTCTCTATGGATTGCCTATTTTGGATA
TTTCATATACATAGAATCATAAANTAAAAA

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FIGURE 372

MCIRQLKFFTTACVCECPQNILSPQPSCVNLGMMWTWALWMLPSLCKFSLAALPAKPENI
SCVYYYRKNLTCTWSPGKETS YTQYTVKR TYAFGEKHDNCTTNSSTSEN RASCSFFLPRI
TIPDNYTIEVEAENG DGVIKSHMTYWRLENI AKTEPPKIFRVKPV LGIKRMIQIEWIKPE
LAPVSSDLKYTLRFRTVNSTSWMEVNF AKNRKDKNQTYNLTGLQPFTEYVIALRCAVKES
KFWSDWSQEKMGMT EEEAPCGLELWRVLKPAEADGRRPVRL L WKKARGAPVLEKTLGYNI
WYYPESNTNLTETMNTTNQQLHLGGESFWVSMISYNSLGKSPVATLRIPAIQEKS FQC
IEVMQACVAEDQLVVKWQSSALDVNTWMI EWFPD VDSEPTTLSWESVSQATNWTIQQDKL
KPFWCYNISVYPMLHDKVGE PYSIQAYAKEGVPSEGPETKVENIGVKT VTTITWKEI PKSE
RKGIIICNYTIFYQAE GKGFC KHAHSEVEKNPKPQIDAMDRPVVGM APPSHCDLQPGMNH
LASLNLSENGAKSTHLLGFWGLNESEVTV PERRVLRKWKELL

Important features of the protein:**Signal peptide:**

1-46

Transmembrane domain:

None

N-glycosylation site:

59-63, 69-73, 99-103, 103-107, 125-129, 198-202, 215-219, 219-223, 309-313, 315-319, 412-416, 427-431, 487-491, 545-549, 563-567

N-myristoylation site:

32-38, 137-143, 483-489, 550-556, 561-567

Amidation site:

274-278

Growth factor and cytokines receptors family signature 1:

62-75

Fibronectin type III domain:

54-144

154-247

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FIGURE 373

CCAGGTCCAACCTGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCC
CTCGACCTCGACCCACGCGTCCGCCAAGCTGGCCCTGCACGGCTGCAAGGGAGGCTCCTG
TGGACAGGCCAGGCAGGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGC
CCCAGCAAGGGCTAGGGTCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCAC
GCCTGGGCTCCAGCAGCATCAGCAGCCCCCAGGACCGGGGGAGGCACAGGTGGCCCCCAC
CACCCGGAGGAGCAGCTCCTGCCCCCTGTCCGGGGGATGACTGATTCTCCTCCGCCAGGCC
ACCCAGAGGAGAAGGCCACCCCGCTGGAGGCACAGGCCATGAGGGGCTCTCAGGAGGTG
CTGCTGATGTGGCTTCTGGTGTGGCAGTGGGCGGCACAGAGCACGCCTACCGGCCCGGC
CGTTAGGGTGTGTGCTGTCCCGGGCTCACGGGGACCCGTGTCTCCGAGTCGTTTCGTGCAGC
GTGTGTACCAGCCCTTCCTCACACCTGCGACGGGCACCGGGCCTGCAGCACCTACCGAA
CCATTTATAGGACCGCCTACCGCCGCAGCCCTGGGCTGGCCCCCTGCCAGGCCTCGCTACG
CGTGCTGCCCCGGCTGGAAGAGGACCAGCGGGCTTCCTGGGGCCTGTGGAGCAGCAATAT
GCCAGCCGCCATGCCGGAACGGAGGGAGCTGTGTCCAGCCTGGCCGCTGCCGCTGCCCTG
CAGGATGGCGGGGTGACACTTGCCAGTCAGATGTGGATGAATGCAGTGCTAGGAGGGGCG
GCTGTCCCAGCGCTGCATCAACACCGCCGGCAGTTACTGGTGCCAGTGTGGGAGGGGC
ACAGCCTGTCTGCAGACGGTACACTCTGTGTGCCCAAGGGAGGGCCCCCAGGGTGGCCC
CCAACCCGACAGGAGTGGACAGTGCAATGAAGGAAGAAGTGCAGAGGCTGCAGTCCAGGG
TGGACCTGCTGGAGGAGAAGCTGCAGCTGGTGCTGGCCCCACTGCACAGCCTGGCCTCGC
AGGCACTGGAGCATGGGCTCCCGGACCCCGGCAGCCTCCTGGTGCACTCCTTCCAGCAGC
TCGGCCGCATCGACTCCCTGAGCGAGCAGATTTCCTTCTGGAGGAGCAGCTGGGGTCCT
GCTCCTGCAAGAAAGACTCGTGACTGCCAGCGCCCCAGGCTGGACTGAGCCCCTCACGC
CGCCCTGCAGCCCCCATGCCCTGCCCAACATGCTGGGGGTCCAGAAGCCACCTCGGGGT
GACTGAGCGGAAGGCCAGGCAGGGCCTTCCTCCTTTTCTCCTCCCCTTCCCTCGGGAGG
GTCCCCAGACCCTGGCATGGGATGGGCTGGGATTTTTTTTGTGAATCCACCCCTGGCTAC
CCCCACCCTGGTTACCCCAACGGCATCCCAAGGCCAGGTGGGCCCTCAGCTGAGGGAAGG
TACGAGTTCCCCTGCTGGAGCCTGGGACCCATGGCACAGGCCAGGCAGCCCGGAGGCTGG
GTGGGGCCTCAGTGGGGGCTGCTGCCTGACCCCCAGCACATAAAAATGAAACGTGAAAA
AAAGGGCGGCCGCGACTCTAGAGTC
GACCTGCAGAAGCTTGGCCGCCATGGCCCACTTGTTTATTGCAGCTTATAATGGTTACAAAT

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FIGURE 374

MTDSPPPGHPEEKATPPGGTGHEGLSGGAADVASGVGSGRHRARLPARPLGCVLSRAHGD
PVSESFVQRVYQPFLTTCDGHRACSTYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGL
PGACGAAICQPPCRNGGSCVQPGRCRCPAGWRGDTQCSDVDECSARRGGCPQRCINTAGS
YWCQCWEGHSLSADGTL CVPKGGPPRVAPNPTGVDSAMKEEVQRLQSRVDLLEEKQLVL
APLHSLASQALEHGLPDPGSLLVHSFQQLGRIDSLSEQISFLEEQLGSCSCKKDS

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FIGURE 375

Wholemount In Situ with Prol449 Orthologue

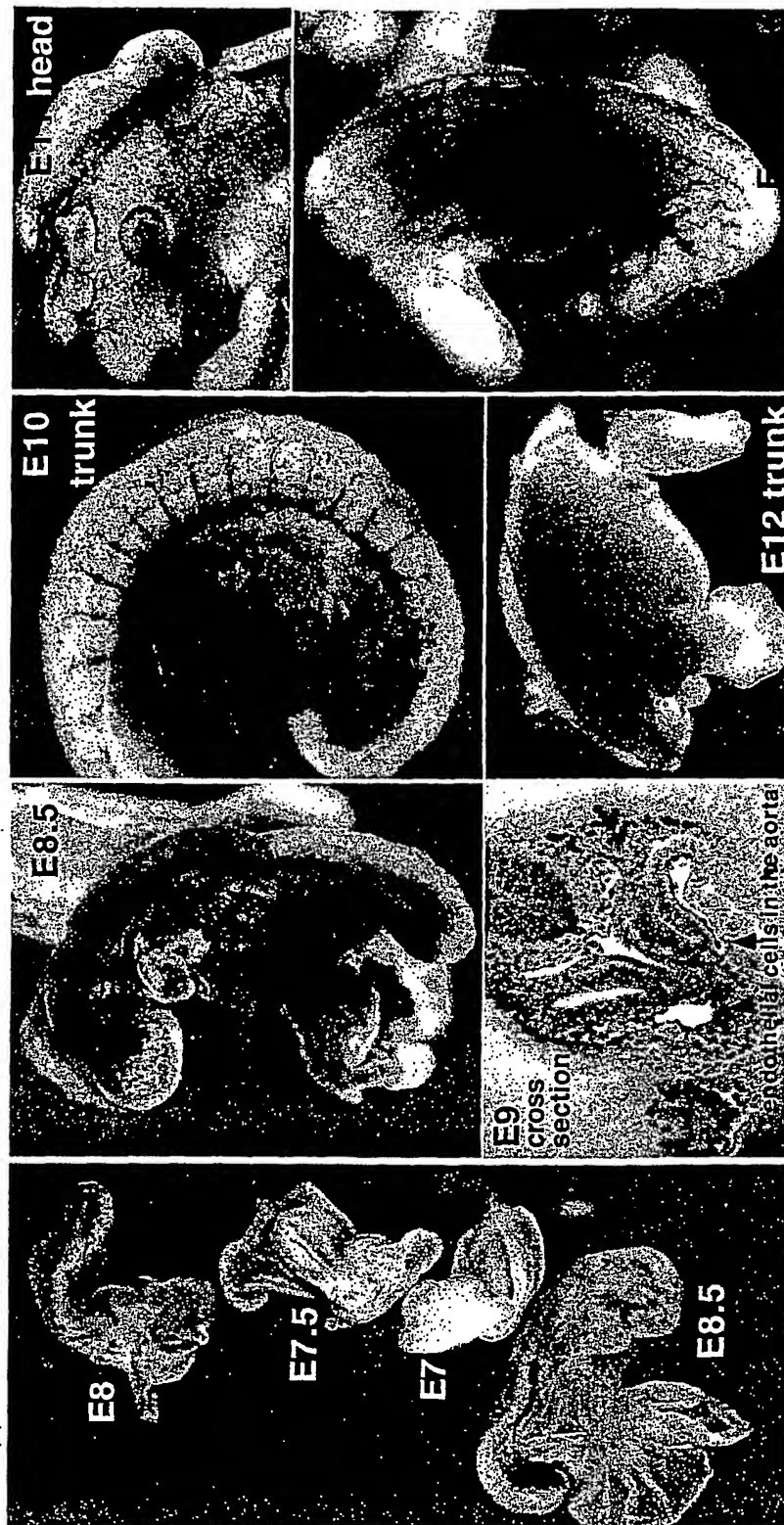
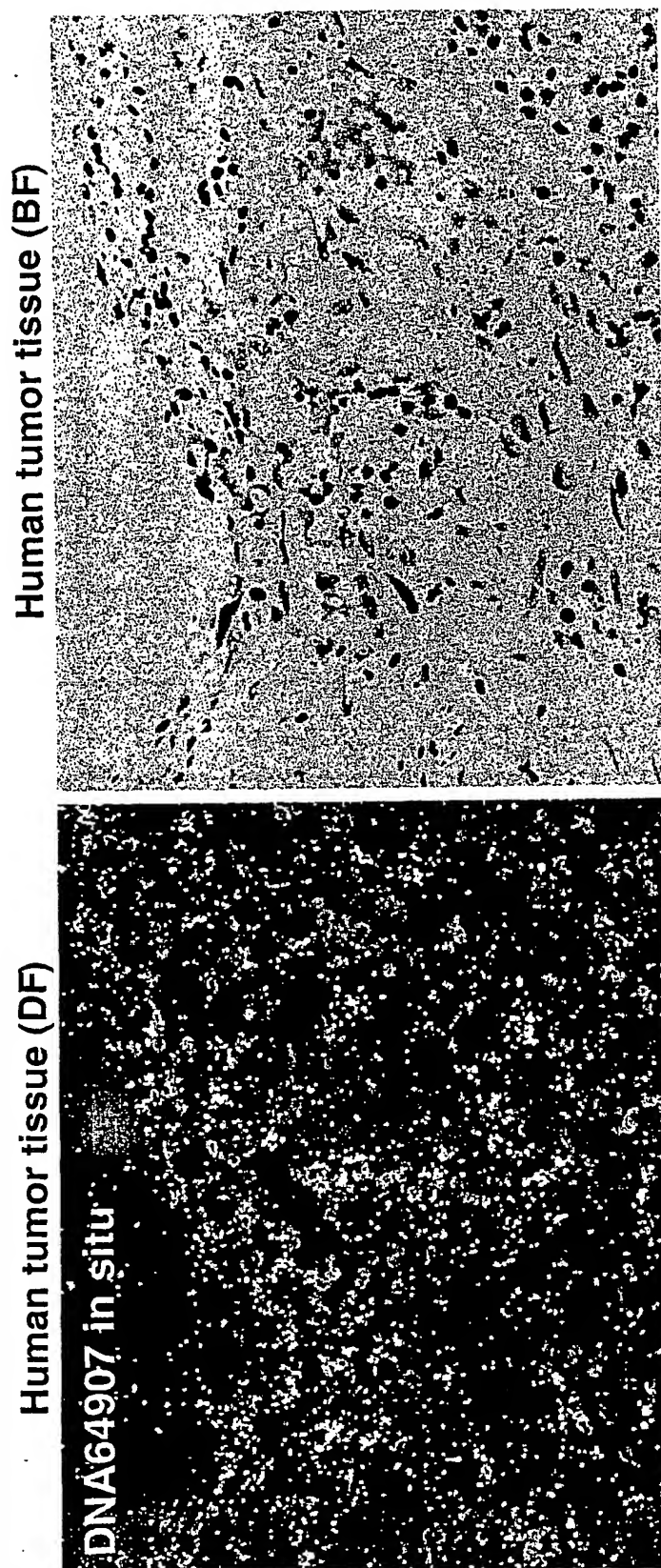


FIGURE 376

PRO1449 is expressed in vasculature of many inflamed and diseased tissues



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FIGURE 377

Mouse orthologue of PRO1449 induces ectopic vessels in the eyes of chicken embryos

